

# DT-3073

## SEQUENCE LISTING

### (1) GENERAL INFORMATION:

(i) APPLICANT: (A) NAME: Kanton Zuerich vertreten durch die Erziehungsdirektion (B) STREET: Walchetur (C) CITY: Zuerich (D) STATE: Zuerich (E) COUNTRY: Switzerland (F) POSTAL CODE (ZIP): CH-8090 (G) TELEPHONE: +41-1-259 2388

(ii) TITLE OF INVENTION: Immunological Detection of Prions

(iii) NUMBER OF SEQUENCES: 9

(iv) COMPUTER READABLE FORM: (A) MEDIUM TYPE: Floppy disk (B) COMPUTER: IBM PC compatible (C) OPERATING SYSTEM: PC-DOS/MS-DOS (D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

(vi) PRIOR APPLICATION DATA: (A) APPLICATION NUMBER: EP 97102837.8 (B) FILING DATE: 21-FEB-1997

### (2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 660 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE: (A) ORGANISM: Bos taurus (D) DEVELOPMENTAL STAGE: Adult

(vii) IMMEDIATE SOURCE: (B) CLONE: pbPrP3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

ATGAAGAAC GACCAAAACC TGGAGGAGGA TGGAACACTG GGGGGAGCCG  
ATACCCAGGA 60

CAGGGCAGTC CTGGAGGCAA CCGTTATCCA CCTCAGGGAG GGGGTGGCTG  
GGGTCAGCCC 120

CATGGAGGTG GCTGGGGCCA GCCTCATGGA GGTGGCTGGG GCCAGCCTCA  
TGGAGGTGGC 180

TGGGGTCAGC CCCATGGTGG TGGCTGGGA CAGCCACATG GTGGTGGAGG  
CTGGGGTCAA 240

GGTGGTACCC ACGGTCAATG GAACAAACCC AGTAAGCCAA AAACCAACAT  
GAAGCATGTG 300

GCAGGAGCTG CTGCAGCTGG AGCAGTGGTA GGGGGCCTTG GTGGCTACAT  
GCTGGGAAGT 360

GCCATGAGCA GGCCTCTTAT ACATTTGGC AGTACTATG AGGACCGTTA  
CTATCGTGAA 420

AACATGCACC GTTACCCCAA CCAAGTGTAC TACAGGCCAG TGGATCAGTA  
TAGTAACCAG 480

AACAACTTG TGCATGACTG TGTCAACATC ACAGTCAAGG AACACACAGT  
CACCAACCACC 540

ACCAAGGGGG AGAACTTCAC CGAAACTGAC ATCAAGATGA TGGAGCGAGT  
GGTGGAGCAA 600

ATGTGCATTA CCCAGTACCA GAGAGAATCC CAGGCTTATT ACCAACGAGG  
GGCAAGTTAA 660

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 219 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE: (A) ORGANISM: Bos taurus

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Met Lys Lys Arg Pro Lys Pro Gly Gly Gly Trp Asn Thr Gly Gly Ser 1

10 15

5

	Arg Tyr Pro Gly Gln Gly Ser Pro Gly Gly Asn Arg Tyr Pro Pro Gln	20
30		25
	Gly Gly Gly Gly Trp Gly Gln Pro His Gly Gly Gly Trp Gly Gln Pro	35
45		40
	His Gly Gly Gly Trp Gly Gln Pro His Gly Gly Gly Trp Gly Gln Pro	50
60		55
	His Gly Gly Gly Trp Gly Gln Pro His Gly Gly Gly Trp Gly Gln Pro	65
75	80	70
	Gly Gly Thr His Gly Gln Trp Asn Lys Pro Ser Lys Pro Lys Thr Asn	85
95		90
	Met Lys His Val Ala Gly Ala Ala Ala Gly Ala Val Val Gly Gly	100
110		105
	Leu Gly Gly Tyr Met Leu Gly Ser Ala Met Ser Arg Pro Leu Ile His	115
125		120
	Phe Gly Ser Asp Tyr Glu Asp Arg Tyr Tyr Arg Glu Asn Met His Arg	130
140		135
	Tyr Pro Asn Gln Val Tyr Tyr Arg Pro Val Asp Gln Tyr Ser Asn Gln	145
155	160	150
	Asn Asn Phe Val His Asp Cys Val Asn Ile Thr Val Lys Glu His Thr	165
175		170
	Val Thr Thr Thr Lys Gly Glu Asn Phe Thr Glu Thr Asp Ile Lys	180
190		185
	Met Met Glu Arg Val Val Glu Gln Met Cys Ile Thr Gln Tyr Gln Arg	195
205		200
	Glu Ser Gln Ala Tyr Tyr Gln Arg Gly Ala Ser	210
	215	

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 33 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid (A) DESCRIPTION: /desc = "oligonucleotide"

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

GGGAATTCCA TATGAAGAAG CGACCAAAAC CTG

33

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 31 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid (A) DESCRIPTION: /desc = "oligonucleotide"

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

CGGGATCCTA TTAAC TTGCC CCTCGTTGGT A

31

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 5 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

Leu Ile His Phe Gly 1                    5

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 9 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Asp Tyr Glu Asp Arg Tyr Tyr Arg Glu 1        5

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 7 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

Gly Ser Asp Tyr Glu Asp Arg 1        5

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 9 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

Tyr Tyr Arg Pro Val Asp Gln Tyr Ser 1        5

(2) INFORMATION FOR SEQ ID NO: 9:

(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 13 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

Cys Ile Thr Gln Tyr Gln Arg Glu Ser Gln Ala Tyr Tyr 1                    5                    10